

SEQUENCE LISTING

<110> Bayer AG

<120> DNA coding for β -tubulin and its use

<130> Le A 33 759

<140>

<141>

<160> 51

<170> PatentIn Ver. 2.1

<210> 1

<211> 1380

<212> DNA

<213> *Cyathostomum coronatum*

<220>

<221> CDS

<222> (1)..(1344)

<400> 1

atg cgt gag atc gtg cat gta caa gct gga caa tgt gga aac caa att 48

Met Arg Glu Ile Val His Val Gln Ala Gly Gln Cys Gly Asn Gln Ile

1

5

10

15

ggg tcc aag ttt tgg gaa gtg atc tct gac gag cat ggc att aag ccc 96

Gly Ser Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Lys Pro

gat ggc aca tac cac gga gaa tct gat cta caa tta gaa cga atc aat 144
Asp Gly Thr Tyr His Gly Glu Ser Asp Leu Gln Leu Glu Arg Ile Asn

35

40

45

gtg tac tat aat gaa gca cat gga ggc aaa tat gtc cca cgt gca gtt 192
Val Tyr Tyr Asn Glu Ala His Gly Gly Lys Tyr Val Pro Arg Ala Val

50

55

60

ctt gtt gat ctc gag ccc gga act atg gat tcc gtc cgt tcc ggg cca 240
Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro

65

70

75

80

tac ggg caa ttg ttc cgc cct gat aac tac gtg ttt gga cag tct ggc 288
Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr Val Phe Gly Gln Ser Gly

85

90

95

gca gga aat aac tgg gca aaa ggt cac tac act gaa ggc gct gaa ctt 336
Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu

100

105

110

gtc gac aat gta cta gat gta gtg cga aaa gaa gca gaa gga tgt gac 384
Val Asp Asn Val Leu Asp Val Val Arg Lys Glu Ala Glu Gly Cys Asp

115

120

125

tgt ctg cag ggc ttc cag cta act cac tca ctt gga gga ggt acc ggt 432
Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly

130

135

140

tcg ggt atg ggc act ctc ctc atc tcc aaa att cgg gag gag tat cct 480

Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro

145 150 155 160

gat aga atc atg tcc tcg ttc tcc gtt gtc ccc tca cca aag gtc tcc 528

Asp Arg Ile Met Ser Ser Phe Ser Val Val Pro Ser Pro Lys Val Ser

165 170 175

gac act gtt gtg gag cct tac aat gct acc cta tcc gtt cat cag ttg 576

Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu

180 185 190

gtt gaa aat aca gac gag act tat tgt att gac aat gaa gcc ctg tat 624

Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr

195 200 205

gat att tgc ttc cgc act ttg aaa ctc acg aac cca act tat gga gat 672

Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Asn Pro Thr Tyr Gly Asp

210 215 220

ctg aat cat ctt gtg tct gta aca atg tct ggt gtc acc aca tgt ctt 720

Leu Asn His Leu Val Ser Val Thr Met Ser Gly Val Thr Thr Cys Leu

225 230 235 240

cgc ttc cct ggc caa ttg aat gcc gat cta cgc aaa cta gct gtt aac 768

Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn

245 250 255

atg gtt cca ttc cct cgt ctt cac ttc ttc atg cct ggt ttt gct ctt 816

Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro

260 265 270

ctt tct gct aaa ggt gct cag gct tac cgt gct ctt acc gta gcc gag 864

Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg Ala Leu Thr Val Ala Glu

275

280

285

ctt aca cag cag atg ttt gat gct aag aat atg atg gct gct tgc gac 912

Leu Thr Gln Gln Met Phe Asp Ala Lys Asn Met Met Ala Ala Cys Asp

290

295

300

cct cga cat gga cgt tat ctc acc gtc gca gcc atg ttc cga gga aga 960

Pro Arg His Gly Arg Tyr Leu Thr Val Ala Ala Met Phe Arg Gly Arg

305

310

315

320

atg agc atg agg gaa gta gac gac cag atg atg tca gtg cag aac aag
1008

Met Ser Met Arg Glu Val Asp Asp Gln Met Met Ser Val Gln Asn Lys

325

330

335

aac tcc tca tac ttc gta gag tgg atc ccg aac aac gtg aag acc gct
1056

Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Thr Ala

340

345

350

gta tgc gac atc ccg cca cga gga ctg aag atg gcc gct acc ttc gtt
1104

Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ala Ala Thr Phe Val

355

360

365

gga aac tca act gcc atc caa gag ctg ttc aag cgc att tca gaa caa
1152

Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln

370

375

380

ttt aca gcc atg ttc cgc cgc aaa gcg ttc ttg cat tgg tac act ggt
1200

Phe Thr Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly

385 390 395 400

gaa ggt atg gac gag atg gag ttc act gaa gca gag tcc aac atg aat
1248

Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn

405 410 415

gat ctc atc tcc gag tac caa cag tac cag gaa gcc acc gct gac gac
1296

Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln Glu Ala Thr Ala Asp Asp

420 425 430

atg ggc gat ctt gat gcg gaa ggc gct gaa gag gct tat cct gag gaa
1344

Met Gly Asp Leu Asp Ala Glu Gly Ala Glu Glu Ala Tyr Pro Glu Glu

435 440 445

taaaccagca gatcgtgttg cgttgttcgt ttctct
1380

<210> 2

<211> 448

<212> PRT

<213> Cyathostomum coronatum

<400> 2

Met Arg Glu Ile Val His Val Gln Ala Gly Gln Cys Gly Asn Gln Ile

1 5 10 15

Gly Ser Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Lys Pro

20 25 30

Asp Gly Thr Tyr His Gly Glu Ser Asp Leu Gln Leu Glu Arg Ile Asn
 35 40 45

Val Tyr Tyr Asn Glu Ala His Gly Gly Lys Tyr Val Pro Arg Ala Val
 50 55 60

Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro
 65 70 75 80

Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr Val Phe Gly Gln Ser Gly
 85 90 95

Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu
 100 105 110

Val Asp Asn Val Leu Asp Val Val Arg Lys Glu Ala Glu Gly Cys Asp
 115 120 125

Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly
 130 135 140

Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro
 145 150 155 160

Asp Arg Ile Met Ser Ser Phe Ser Val Val Pro Ser Pro Lys Val Ser
 165 170 175

Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu
 180 185 190

Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr

195

200

205

Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Asn Pro Thr Tyr Gly Asp

210

215

220

Leu Asn His Leu Val Ser Val Thr Met Ser Gly Val Thr Thr Cys Leu

225

230

235

240

Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn

245

250

255

Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro

260

265

270

Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg Ala Leu Thr Val Ala Glu

275

280

285

Leu Thr Gln Gln Met Phe Asp Ala Lys Asn Met Met Ala Ala Cys Asp

290

295

300

Pro Arg His Gly Arg Tyr Leu Thr Val Ala Ala Met Phe Arg Gly Arg

305

310

315

320

Met Ser Met Arg Glu Val Asp Asp Gln Met Met Ser Val Gln Asn Lys

325

330

335

Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Thr Ala

340

345

350

Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ala Ala Thr Phe Val

355

360

365

Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln

370

375

380

Phe Thr Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly

385

390

395

400

Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn

405

410

415

Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln Glu Ala Thr Ala Asp Asp

420

425

430

Met Gly Asp Leu Asp Ala Glu Gly Ala Glu Glu Ala Tyr Pro Glu Glu

435

440

445

<210> 3

<211> 1429

<212> DNA

<213> *Cylicocyclus nassatus*

<220>

<221> CDS

<222> (1) .. (1362)

<400> 3

aag ttc tct act gca ata atg cgt gag atc gtg cat gta caa gct gga 48

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

1

5

10

15

car tgt gga aac caa att ggy tcc aag tty tgg gaa gtg atc tct gac 96
Gln Cys Gly Asn Gln Ile Xaa Ser Lys Phe Trp Glu Val Ile Ser Asp

20

25

30

gag cac ggc att aag ccy gay ggc aca tac cay gga gaa tct gay yta 144
Glu His Gly Ile Lys Xaa Asp Gly Thr Tyr His Gly Glu Ser Asp Xaa

35

40

45

caa tta gaa cga atc aat gtg tac tat aat gaa gca cat gga ggc aar 192
Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50

55

60

tat gtc ccg cgt gca gtt ctt gtt gat ctc gag ccc gga act atg gat 240
Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65

70

75

80

tcr gtc cgy tcy ggg cca tac ggg caa ttg ttc cgc cct gat aac tac 288
Xaa Val Xaa Xaa Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85

90

95

gtg ttt gga cag tct ggc gca gga aat aac tgg gca aaa ggt cac tac 336
Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100

105

110

act gaa ggy gct gaa ctt gtc gac aat gta cta gat gta gtg cga aaa 384
Thr Glu Xaa Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115

120

125

gaa gct gaa gga tgt gac tgt ctg cag ggc ttc cag cta act cac tca 432

255

cgt aaa cta gct gtt aac atg gyt cca ttc cct cgt ctt cac tty tty 816
 Arg Lys Leu Ala Val Asn Met Xaa Pro Phe Pro Arg Leu His Phe Phe
 260 265 270

atg cct ggc ttt gct ccc ctc tct gcy aaa ggc gcy cag gct tac cgt 864
Met Pro Gly Phe Ala Pro Leu Ser Xaa Lys Gly Xaa Gln Ala Tyr Arg
275 280 285

gct ctt act gta gcc gag ctw acy caa yag atg ttc gat gcc aaa aat 912
Ala Leu Thr Val Ala Glu Xaa Xaa Gln Xaa Met Phe Asp Ala Lys Asn
290 295 300

atg atg gcc gct tgc gac cct cga cat gga crt tat ctc acc gty gca 960
Met Met Ala Ala Cys Asp Pro Arg His Gly Xaa Tyr Leu Thr Xaa Ala
305 310 315 320

gcc atg ttc cga gga cga atg agc ayg agg gar gta gac gac cag atg
1008

Ala Met Phe Arg Gly Arg Met Ser Xaa Arg Glu Val Asp Asp Gln Met

325 330 335

atg tca gtg cag aac aag aac tcc tca tac ttc gta gag tgg att ccg
1056

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro

340 345 350

aac aac gtc aar acc gcy gta tgc gac att ccg ccr aga gga ctg aaa
1104

Asn Asn Val Lys Thr Xaa Val Cys Asp Ile Pro Xaa Arg Gly Leu Lys

355 360 365

atg gcc gct acc ttc gtt gga aac yca act gcc aty caa gag ctg tty
1152

Met Ala Ala Thr Phe Val Gly Asn Xaa Thr Ala Xaa Gln Glu Leu Phe

370

375

380

aag cgc att tca gaa caa tty aca gct atg ttc cgc cgc aaa gcg tty
1200

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

390

395

400

ttg cat ygg tay act ggw gaa ggt atg gay gag atg gag ttc act gaa
1248

Leu His Xaa Tyr Thr Xaa Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

410

415

gcc gag tcc aac atg aat gat ctc atc tcc gaa tac car caa tac cag
1296

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

gaa gct acm gct gac gat atg ggc gat ctc gat gcg gaa ggc gct gaa
1344

Glu Ala Xaa Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

gag gct tac cct gar gaa tagamcagca gaytgtgttg cgttgttcgt
1392

Glu Ala Tyr Pro Glu Glu

450

ttctctrtgt caatgcgaaa tacacattga ttgcgtt
1429

<210> 4

<211> 454

<212> PRT

<213> Cylicocyclus nassatus

<400> 4

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1 5 10 15

Gln Cys Gly Asn Gln Ile Xaa Ser Lys Phe Trp Glu Val Ile Ser Asp

20 25 30

Glu His Gly Ile Lys Xaa Asp Gly Thr Tyr His Gly Glu Ser Asp Xaa

35 40 45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50 55 60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65 70 75 80

Xaa Val Xaa Xaa Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85 90 95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100 105 110

Thr Glu Xaa Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115 120 125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser

130 135 140

Leu Gly Gly Gly Thr Gly Ser Xaa Met Gly Xaa Leu Leu Ile Xaa Lys

145 150 155 160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Xaa Ser Ser Phe Xaa Val Val

165 170 175

Pro Ser Pro Lys Val Xaa Asp Xaa Val Val Glu Pro Tyr Asn Ala Thr

180 185 190

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Xaa Cys Ile

195 200 205

Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Xaa Xaa Lys Leu Xaa

210 215 220

Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser

225 230 235 240

Xaa Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Xaa Ala Asp Xaa

245 250 255

Arg Lys Leu Ala Val Asn Met Xaa Pro Phe Pro Arg Leu His Phe Phe

260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Xaa Lys Gly Xaa Gln Ala Tyr Arg

275 280 285

Ala Leu Thr Val Ala Glu Xaa Xaa Gln Xaa Met Phe Asp Ala Lys Asn

290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Xaa Tyr Leu Thr Xaa Ala

305

310

315

320

Ala Met Phe Arg Gly Arg Met Ser Xaa Arg Glu Val Asp Asp Gln Met

325

330

335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro

340

345

350

Asn Asn Val Lys Thr Xaa Val Cys Asp Ile Pro Xaa Arg Gly Leu Lys

355

360

365

Met Ala Ala Thr Phe Val Gly Asn Xaa Thr Ala Xaa Gln Glu Leu Phe

370

375

380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

390

395

400

Leu His Xaa Tyr Thr Xaa Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

410

415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

Glu Ala Xaa Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

Glu Ala Tyr Pro Glu Glu

450

<210> 5

<211> 1428

<212> DNA

<213> *Cylicocyclus nassatus*

<220>

<221> CDS

<222> (1) .. (1362)

<400> 5

aag ttc tct act gca ata atg cgt gag atc gtg cat gta caa gct gga 48

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1 5 10 15

cag tgt gga aac caa att ggc tcc aag ttt tgg gaa gtg atc tct gac 96

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp

20 25 30

gag cac ggc att aag cct gat ggc aca tac cac gga gaa tct gat tta 144

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu

35 40 45

caa tta gaa cga atc aat gtg tac tat aat gaa gca cat gga ggc aaa 192

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50 55 60

tat gtc ccg cgt gca gtt ctt gtt gat ctc gag ccc gga act atg gat 240

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65 70 75 80

tcg gtc cgt tcc ggg cca tac ggg caa ttg ttc cgc cct gat aac tac 288

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85

90

95

gtg ttt gga cag tct ggc gca gga aat aac tgg gca aaa ggt cac tac 336

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100

105

110

act gaa ggc gct gaa ctt gtt gac aat gta cta gat gta gtg cga aaa 384

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115

120

125

gaa gct gaa gga tgt gac tgt ctg cag ggc ttc cag cta act cac tca 432

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser

130

135

140

ctt gga gga ggt acc gga tcg ggt atg ggc act ctc ctc atc tcc aaa 480

Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys

145

150

155

160

att cgg gag gag tat cct gat aga atc atg tcc tcg ttc tcc gtt gtt 528

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Ser Ser Phe Ser Val Val

165

170

175

ccc tca cca aag gtc tcc gac acc gtt gtg gag ccg tac aat gct acc 576

Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr Asn Ala Thr

180

185

190

cta tcc gtt cat cag ttg gtt gaa aat aca gac gag act ttc tgt att 624

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile

195

200

205

335

1056

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro

340

345

350

1104

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys

355

360

365

1152

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe

370

375

380

1200

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

390

395

400

1248

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

410

415

1296

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

1344

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

1392

Glu Ala Tyr Pro Glu Glu

450

tctctgtgtc aatgcgaaat acacattgat tgcggt
1428

<210> 6

<211> 454

<212> PRT

<213> Cylicocyclus nassatus

<400> 6

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1

5

10

15

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp

20

25

30

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu

35

40

45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50

55

60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65

70

75

80

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85

90

95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100

105

110

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115

120

125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser

130

135

140

Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys

145

150

155

160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Ser Ser Phe Ser Val Val

165

170

175

Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr Asn Ala Thr

180

185

190

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile

195

200

205

Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr

210

215

220

Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser

225

230

235

240

Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu

245

250

255

Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe
 260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg
 275 280 285

Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn
 290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala
 305 310 315 320

Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met
 325 330 335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro
 340 345 350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys
 355 360 365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe
 370 375 380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe
 385 390 395 400

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu
 405 410 415

3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

Glu Ala Tyr Pro Glu Glu

450

<210> 7

<211> 1429

<212> DNA

<213> *Cylicocyclus nassatus*

<220>

<221> CDS

<222> (1) .. (1362)

<400> 7

aag ttc tct act gca ata atg cgt gag atc gtg cat gta caa gct gga 48

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1

5

10

15

cag tgt gga aac caa att ggt tcc aag ttt tgg gaa gtg atc tct gac 96

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp

20

25

30

gag cac ggc att aag ccc gat ggc aca tac cac gga gaa tct gac tta 144

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu

att cgg gag gag tat cct gat aga atc ata tcc tcg ttc ttc gtt gtt 528

285

ttg cat tgg tat act ggt gaa ggt atg gac gag atg gag ttc act gaa
1248

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu
405 410 415

gcc gag tcc aac atg aat gat ctc atc tcc gaa tac caa caa tac cag
1296

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln
420 425 430

gaa gct acc gct gac gat atg ggc gat ctc gat gcg gaa ggc gct gaa
1344

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu
435 440 445

gag gct tac cct gag gaa tagaacagca gattgtgttg cgttgttcgt
1392

Glu Ala Tyr Pro Glu Glu
450

ttctctgtgt caatgcgaaa tacacattga ttgcgtt
1429

<210> 8

<211> 454

<212> PRT

<213> Cylicocyclus nassatus

<400> 8

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly
1 5 10 15

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp

20

25

30

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu

35

40

45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50

55

60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65

70

75

80

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85

90

95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100

105

110

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115

120

125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser

130

135

140

Leu Gly Gly Gly Thr Gly Ser Ser Met Gly Thr Leu Leu Ile Phe Lys

145

150

155

160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Ile Ser Ser Phe Phe Val Val

165

170

175

Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr Asn Ala Thr

180

185

190

Leu	Ser	Val	His	Gln	Leu	Val	Glu	Asn	Thr	Asp	Glu	Thr	Phe	Cys	Ile		
195						200						205					
Asp	Asn	Glu	Ala	Leu	Tyr	Asp	Ile	Cys	Phe	Arg	Thr	Leu	Lys	Leu	Thr		
210						215						220					
Asn	Pro	Thr	Tyr	Gly	Asp	Leu	Asn	His	Leu	Val	Ser	Val	Thr	Met	Ser		
225				230				235				240					
Gly	Val	Thr	Thr	Cys	Leu	Arg	Phe	Pro	Gly	Gln	Leu	Ser	Ala	Asp	Leu		
				245						250						255	
Arg	Lys	Leu	Ala	Val	Asn	Met	Val	Pro	Phe	Pro	Arg	Leu	His	Phe	Phe		
260								265								270	
Met	Pro	Gly	Phe	Ala	Pro	Leu	Ser	Ala	Lys	Gly	Ala	Gln	Ala	Tyr	Arg		
275						280						285					
Ala	Leu	Thr	Val	Ala	Glu	Leu	Thr	Gln	Gln	Met	Phe	Asp	Ala	Lys	Asn		
290				295				300				305					
Met	Met	Ala	Ala	Cys	Asp	Pro	Arg	His	Gly	Arg	Tyr	Leu	Thr	Val	Ala		
305				310				315				320					
Ala	Met	Phe	Arg	Gly	Arg	Met	Ser	Met	Arg	Glu	Val	Asp	Asp	Gln	Met		
				325						330						335	
Met	Ser	Val	Gln	Asn	Lys	Asn	Ser	Ser	Tyr	Phe	Val	Glu	Trp	Ile	Pro		
340						345						350					

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys

355

365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe

370

380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

395

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

445

Glu Ala Tyr Pro Glu Glu

450

<210> 9

<211> 1428

<212> DNA

<213> Cylicocyclus nassatus

<220>

<221> CDS

<222> (1) .. (1362)

act gaa ggc gct gaa ctt gtc gac .aat gta cta gat gta gtg cga aaa 384

240

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys

355

360

365

atg gcc gct acc ttc gtt gga aac tca act gcc att caa gag ctg ttc
1152

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe

370

375

380

aag cgc att tca gaa caa ttc aca gct atg ttc cgc cgc aaa gcg ttc
1200

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

390

395

400

ttg cat tgg tat act ggt gaa ggt atg gac gag atg gag ttc act gaa
1248

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

410

415

gcc gag tcc aac atg aat gat ctc atc tcc gaa tac cag caa tac cag
1296

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

gaa gct acc gct gac gat atg ggc gat ctc gat gcg gaa ggc gct gaa
1344

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

gag gct tac cct gaa gaa tagacagcag attgtgttgc gttgttcggt
1392

Glu Ala Tyr Pro Glu Glu

450

tctctgtgtc aatgcgaaat acacattgat tgcggt
1428

<210> 10

<211> 454

<212> PRT

<213> Cylicocyclus nassatus

<400> 10

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly

1 5 10 15

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp

20 25 30

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu

35 40 45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys

50 55 60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp

65 70 75 80

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr

85 90 95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr

100 105 110

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys

115 120 125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser

130

140

Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys

145

155

160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Ser Ser Phe Ser Val Val

165

175

Pro Ser Pro Lys Val Phe Asp Thr Val Val Glu Pro Tyr Asn Ala Thr

180

190

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile

195

205

Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr

210

220

Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser

225

235

240

Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu

245

255

Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe

260

270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg

275

285

Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn

290

295

300

Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala

305

310

315

320

Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met

325

330

335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro

340

345

350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys

355

360

365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe

370

375

380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe

385

390

395

400

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu

405

410

415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln

420

425

430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu

435

440

445

Glu Ala Tyr Pro Glu Glu

450

<220>

<221> intron

<222> (1915)..(1966)

<220>

<221> intron

<222> (2064)..(2119)

<220>

<221> intron

<222> (2306)..(2354)

<220>

<221> intron

<222> (2475)..(2523)

<220>

<221> intron

<222> (2592)..(2655)

<400> 11

aagttctcta ctgcaataat gcgtgagatc gtgcatgtac aagctggaca rtgtggaaac 60
 caaattgggtt ccaaggtrcg gtagtttyrr twktytrytg atcgtaattc sggmgtytytr 120
 dagtrrryttt ttycgytggy ratgttgcat yrtgttgcga taaascyraa aawtcawwag 180
 rcgaggctgt aaaagsactt ytacttttra atmcrytgta gcagcatgag tcatcrgcat 240
 gtttgcagtg sgttttttat gcgcwgawcc ytcagaaga tgagaatgcy wtccaytgag 300
 cwtagartct grctttctct cgttawctaa ratcaamtta carcrytyca ttttkcagtt 360
 ytgggaagtg atctctgacg agcacggcat taagccygay ggcacatacc ayggagaatc 420
 tgatytacaa ttagaacgaa tcaatgtgta ctataatgaa gcacatgggtt agtcgtayat 480
 ccgcttcggtt gtytcccmat gcagrccyct tcagttttta taactgycga aatatcgatc 540

gggctctttt gcagcggccw ygattacgca ataccayygc ygcygcagtg gcrgtcgaaa 600
 ttaatgtggt caracgtgaa aatgtggtgc tttttaggagg caartatgtc ccgcgtgcag 660
 ttcttgttga tctcgagccc ggaactatgg attcgggtccg ytccggggcca tacggggcaat 720
 tgttccgccc tgataactac gtgtttggac agtctggcgc aggaaataac tgggcaaaag 780
 gtcactacac tgaaggygct gaacttgtcg acaatgtact agatgtagtg cgaaaagaag 840
 ctgaaggatg tgactgtctg caggtaaatt tccaagtagt agcaggaaat ggtwtgtgra 900
 tagcataaca aaagtcatag aaggaatatg gacgctagtc aaaacaaagw tggacgttar 960
 tcggctgtcc gggacarttt ggaagtcatg ggtcasccaa cacgcttttt tamaagtaca
 1020
 tcatactctt ttcccacgaa aagctatttt gcgtattacg gggtagaggg gaggggtcaa
 1080
 aatcacagat tgctgaaaty tggttcactg ragttattgr tgaaaatcat attgattttg
 1140
 cttgtactg ccttcttttr aggctatgct ttacaatctt ggggcctgga taaccgaatt
 1200
 gtcygaagtt tttcggatc caccgacggg gaaggggcat artatcgta kttcttgkta
 1260
 tttcgcagca tatggcaatc tytccacttc tgacaagttt tcygtagaaa atatwcttca
 1320
 aggtstcaag aacyttgctg ctargrctgt aaaccaayct gtatcycttt cagggtcttc
 1380
 agctaactca ctacttgga ggaggtaccg gatcgggtat gggcactctc ctcatctcca
 1440
 aaattcggga ggagtatcct gatagaatca tgtcctcggt ctccgttggt cctcaccaa
 1500
 aggtctccga caccgttggt gagccgtaca atgctaccct atccgttcat cagttgggtg
 1560
 aaaatacaga cgaracttwc tgtattgaca atgaagctct ttatgatatt tgcttccgca
 1620
 cyytgaaact cacsaaacca acttatggag atctgaatca tcttggttrg yrayatkcsa
 1680
 ytgtgagct tdgtrgaatt tvctaattwt ktyhamtdty yagtggtctg aacaatgtct
 1740
 ggygtcacta catgycttcg ctccctggc caattgrayg ccgatctwgc taaactagct
 1800
 gttaacatgg ytccattccc tcgtcttcac ttttyatgc ctggctttgc tcccctctct
 1860
 gcyaaaggcg cycaggctta ccgtgctctt actgtagccg agctwacyca rcagggtgcgt
 1920

ctgcttater ttgwtgayrt gtgtttattc kttgtrtatt ttayagatgt tcgatgccaa
1980

aaatatgatg gccgcttgcg accctcgaca tggacrttat ctcaccgtyg cagccatggt
2040

ccgaggacga atgagcayga gggtaagtgg mtkmttggyg ytytaryaya rctcrgacga
2100

awtgctgtta tgtcmtagga rgtagacgac cagatgatgt cagtgcagaa caagaactcc
2160

tcatacttcg tagagtggat tccgaacaac gtcaaraccg cygtatgcga cattccgccc
2220

agaggactga aaatggccgc taccttcgtt ggaaacycaa ctgccatcca agagctgtty
2280

aagcgcattt cagaacaatt yacaggttdg tttgtgcaya ttatggtgaa agcagattar
2340

ttgcgaygtt gcagctatgt tccgccgcaa agcgtyttg catygggaya ctggwgaagg
2400

tatggaygag atggagttca ctgaagccga gtccaacatg aatgatctca tctccgaata
2460

ccarcaatac caggttcggc tgtytttcwt rgayactgtr ttttaataatt wtyttgtct
2520

aggaagctac cgctgacgat atgggcgatc tcgatgcgga aggcgctgaa gaggcttacc
2580

ctgargaata gamcagcaga ytgtgttgcg ttgttcgttt ctctrtgtca atgcgaaata
2640

cacattgatt gcgtt
2655

<210> 12

<211> 23

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: hybridization probe/primer

<400> 12

[illegible]

<211> 20

<213> Synthetic sequence

<223> Description of the synthetic

<400> 13

20

<211> 37

<213> Synthetic sequence

<223> Description of the synthetic

<400> 14

37

<211> 22

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 15

gaccgctgta tgcgacattc cg

22

<210> 16

<211> 22

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 16

aactcaactg ccatccaaga gc

22

<210> 17

<211> 21

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 17

gctatgttcc gccgcaaagc g

21

<210> 18

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 18

acgagcacgg cattaagcct gatgg

25

<210> 19

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 19

ccatcaggct taatgccgtg ctcgt

25

<210> 20

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 20

ccgaatccat agttccgggc tcgag

25

<210> 21

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 21

ccgacaccgt tgtggagccg taca

24

<210> 22

<211> 25

<212> DNA

<213> Synthetic sequence

<400> 24

tgttccgagg acgaatgagc atgag

25

<210> 25

<211> 25

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 25

ctcatgctca ttcgtcctcg gaaca

25

<210> 26

<211> 26

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 26

aggtagacga ccagatgatg tcagtg

26

<210> 27

<211> 26

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 27

cactgacatc atctggctgt ctacct

26

<210> 28

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 28

ggcggaatgt cgcatacagc ggtc

24

<210> 29

<211> 26

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic
sequence: primer/hybridization probes

<400> 29

cggagatgag atcattcatg ttggac

<210> 30

<211> 24

<212> DNA

<213> Synthetic sequence

$\langle 220 \rangle$

```
<223> Description of the synthetic
sequence: primer/hybridization probes
```

<400> 30

ctctcctcat ctccaaaatt cggg

<210> 31

<211> 25

<212> DNA

<213> Synthetic sequence

$\langle 220 \rangle$

```
<223> Description of the synthetic
      sequence: primer/hybridization probes
```

<400> 31

cagctaactc actcacttgg aggag

25

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 34

ggttgaaaat acagacgaga cttta

24

<210> 35

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 35

aaagagcttc attgtcaata caga

24

<210> 36

<211> 23

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 36

caattggcca gggaagcgaa gac

23

<210> 37

<211> 23

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 37

gtcttcgctt ccctggccaa ttg

23

<210> 38

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 38

cctggctttg ctccccctctc tgct

24

<210> 39

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 39

agcagagagg ggagcaaagc cagg

24

<210> 40

<211> 23

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 40

aacgcaatca atgtgtattt cgc

23

<210> 41

<211> 18

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 41

cccgacggca cataccat

18

<210> 42

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 42

gaaacgaaca acgcaacaca atct

24

<210> 43

<211> 22

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 43

caagctggac aatgtggaaa cc

22

<210> 44

<211> 22

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 44

yagagaaacg aacaacgcaa ca

22

<210> 45

<211> 23

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 45

ttgatctcga gcccggaact atg

23

<210> 46

<211> 22

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 46

tctcgagccc ggaactatgg at

22

<210> 47

<211> 24

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 47

cccgaatttt ggagatgagg agag

24

<210> 48

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 48

ggncartgyg gnaaycarat

20

<210> 49

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 49

gaytgyytnc arggnttyca

20

<210> 50

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 50

tgraanceyt gnarrcartc

20

<210> 51

<211> 20

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic

sequence: primer/hybridization probes

<400> 51

tcytgrtayt gytgrtaytc

20

SEQUENCE LISTING

<110> Von Samson-Himmelstjerna, Georg
Harder, Achim
Schneider, Thomas
Pape, Michaela

<120> DNA Coding for Beta-Tubulin and Use Thereof

<130> Mo6878/LeA 33 759

<140> US 10/030,566

<141> 2002-01-07

<150> PCT/EP00/06104

<151> 2000-06-30

<150> DE19931883.2

<151> 1999-07-09

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1380

<212> DNA

<213> Cyathostomum coronatum

<220>

<221> CDS

<222> (1)..(1344)

<223>

<400> 1

atg	cgt	gag	atc	gtg	cat	gta	caa	gct	gga	caa	tgt	gga	aac	caa	att	48
Met	Arg	Glu	Ile	Val	His	Val	Gln	Ala	Gly	Gln	Cys	Gly	Asn	Gln	Ile	
1				5					10					15		

ggt	tcc	aag	ttt	tgg	gaa	gtg	atc	tct	gac	gag	cat	ggc	att	aag	ccc	96
Gly	Ser	Lys	Phe	Trp	Glu	Val	Ile	Ser	Asp	Glu	His	Gly	Ile	Lys	Pro	
			20					25					30			

gat	ggc	aca	tac	cac	gga	gaa	tct	gat	cta	caa	tta	gaa	cga	atc	aat	144
Asp	Gly	Thr	Tyr	His	Gly	Glu	Ser	Asp	Leu	Gln	Leu	Glu	Arg	Ile	Asn	
		35					40					45				

gtg	tac	tat	aat	gaa	gca	cat	gga	ggc	aaa	tat	gtc	cca	cgt	gca	gtt	192
Val	Tyr	Tyr	Asn	Glu	Ala	His	Gly	Gly	Lys	Tyr	Val	Pro	Arg	Ala	Val	
	50					55					60					

ctt	gtt	gat	ctc	gag	ccc	gga	act	atg	gat	tcc	gtc	cgt	tcc	ggg	cca	240
Leu	Val	Asp	Leu	Glu	Pro	Gly	Thr	Met	Asp	Ser	Val	Arg	Ser	Gly	Pro	
65					70				75					80		

tac	ggg	caa	ttg	ttc	cgc	cct	gat	aac	tac	gtg	ttt	gga	cag	tct	ggc	288
Tyr	Gly	Gln	Leu	Phe	Arg	Pro	Asp	Asn	Tyr	Val	Phe	Gly	Gln	Ser	Gly	
				85					90					95		

gca	gga	aat	aac	tgg	gca	aaa	ggt	cac	tac	act	gaa	ggc	gct	gaa	ctt	336
Ala	Gly	Asn	Asn	Trp	Ala	Lys	Gly	His	Tyr	Thr	Glu	Gly	Ala	Glu	Leu	
			100					105					110			



gga aac tca act gcc atc caa gag ctg ttc aag cgc att tca gaa caa 1152
 Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln
 370 375 380

ttt aca gcc atg ttc cgc cgc aaa gcg ttc ttg cat tgg tac act ggt 1200
 Phe Thr Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly
 385 390 395 400

gaa ggt atg gac gag atg gag ttc act gaa gca gag tcc aac atg aat 1248
 Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn
 405 410 415

gat ctc atc tcc gag tac caa cag tac cag gaa gcc acc gct gac gac 1296
 Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln Glu Ala Thr Ala Asp Asp
 420 425 430

atg ggc gat ctt gat gcg gaa ggc gct gaa gag gct tat cct gag gaa 1344
 Met Gly Asp Leu Asp Ala Glu Gly Ala Glu Glu Ala Tyr Pro Glu Glu
 435 440 445

taaaccagca gatcgtgttg cgttgttcgt ttctct 1380

<210> 2
 <211> 448
 <212> PRT
 <213> Cyathostomum coronatum

<400> 2

Met Arg Glu Ile Val His Val Gln Ala Gly Gln Cys Gly Asn Gln Ile
 1 5 10 15

Gly Ser Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Lys Pro
 20 25 30

Asp Gly Thr Tyr His Gly Glu Ser Asp Leu Gln Leu Glu Arg Ile Asn
 35 40 45

Val Tyr Tyr Asn Glu Ala His Gly Gly Lys Tyr Val Pro Arg Ala Val
 50 55 60

Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro
 65 70 75 80

Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr Val Phe Gly Gln Ser Gly
 85 90 95

Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu
 100 105 110

Val Asp Asn Val Leu Asp Val Val Arg Lys Glu Ala Glu Gly Cys Asp
 115 120 125

Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly
 130 135 140

Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro
145 150 155 160

Asp Arg Ile Met Ser Ser Phe Ser Val Val Pro Ser Pro Lys Val Ser
165 170 175

Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu
180 185 190

Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr
195 200 205

Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Asn Pro Thr Tyr Gly Asp
210 215 220

Leu Asn His Leu Val Ser Val Thr Met Ser Gly Val Thr Thr Cys Leu
225 230 235 240

Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn
245 250 255

Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro
260 265 270

Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg Ala Leu Thr Val Ala Glu
275 280 285

Leu Thr Gln Gln Met Phe Asp Ala Lys Asn Met Met Ala Ala Cys Asp
290 295 300

Pro Arg His Gly Arg Tyr Leu Thr Val Ala Ala Met Phe Arg Gly Arg
305 310 315 320

Met Ser Met Arg Glu Val Asp Asp Gln Met Met Ser Val Gln Asn Lys
325 330 335

Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Thr Ala
340 345 350

Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ala Ala Thr Phe Val
355 360 365

Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln
370 375 380

Phe Thr Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly
385 390 395 400

Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn
405 410 415

Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln Glu Ala Thr Ala Asp Asp
420 425 430

Met Gly Asp Leu Asp Ala Glu Gly Ala Glu Glu Ala Tyr Pro Glu Glu
435 440 445

<210>	3
<211>	1429
<212>	DNA
<213>	Cylicocycclus nassatus

```
<220>
<221> CDS
<222> (1)..(1362)
<223> Xaa is a variable amino acid.
```

<400>	3																
aag	ttc	tct	act	gca	ata	atg	cgt	gag	atc	gtg	cat	gta	caa	gct	gga		48
Lys	Phe	Ser	Thr	Ala	Ile	Met	Arg	Glu	Ile	Val	His	Val	Gln	Ala	Gly		
1				5					10					15			
car	tgt	gga	aac	caa	att	ggg	tcc	aag	tty	tgg	gaa	gtg	atc	tct	gac		96
Gln	Cys	Gly	Asn	Gln	Ile	Xaa	Ser	Lys	Phe	Trp	Glu	Val	Ile	Ser	Asp		
			20					25					30				
gag	cac	ggc	att	aag	ccy	gay	ggc	aca	tac	cay	gga	gaa	tct	gay	yta		144
Glu	His	Gly	Ile	Lys	Xaa	Asp	Gly	Thr	Tyr	His	Gly	Glu	Ser	Asp	Xaa		
		35					40					45					
caa	tta	gaa	cga	atc	aat	gtg	tac	tat	aat	gaa	gca	cat	gga	ggc	aar		192
Gln	Leu	Glu	Arg	Ile	Asn	Val	Tyr	Tyr	Asn	Glu	Ala	His	Gly	Gly	Lys		
	50					55					60						
tat	gtc	ccg	cgt	gca	gtt	ctt	gtt	gat	ctc	gag	ccc	gga	act	atg	gat		240
Tyr	Val	Pro	Arg	Ala	Val	Leu	Val	Asp	Leu	Glu	Pro	Gly	Thr	Met	Asp		
65				70					75						80		
tcr	gtc	cgy	tcy	ggg	cca	tac	ggg	caa	ttg	ttc	cgc	cct	gat	aac	tac		288
Xaa	Val	Arg	Xaa	Gly	Pro	Tyr	Gly	Gln	Leu	Phe	Arg	Pro	Asp	Asn	Tyr		
				85					90					95			
gtg	ttt	gga	cag	tct	ggc	gca	gga	aat	aac	tgg	gca	aaa	ggg	cac	tac		336
Val	Phe	Gly	Gln	Ser	Gly	Ala	Gly	Asn	Asn	Trp	Ala	Lys	Gly	His	Tyr		
			100					105					110				
act	gaa	ggg	gct	gaa	ctt	gtc	gac	aat	gta	cta	gat	gta	gtg	cga	aaa		384
Thr	Glu	Xaa	Ala	Glu	Leu	Val	Asp	Asn	Val	Leu	Asp	Val	Val	Arg	Lys		
		115					120					125					
gaa	gct	gaa	gga	tgt	gac	tgt	ctg	cag	ggc	ttc	cag	cta	act	cac	tca		432
Glu	Ala	Glu	Gly	Cys	Asp	Cys	Leu	Gln	Gly	Phe	Gln	Leu	Thr	His	Ser		
	130					135					140						



Xaa Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Xaa Ala Asp Xaa
245 250 255

Arg Lys Leu Ala Val Asn Met Xaa Pro Phe Pro Arg Leu His Phe Phe
260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg
275 280 285

Ala Leu Thr Val Ala Glu Xaa Xaa Gln Xaa Met Phe Asp Ala Lys Asn
290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Xaa Tyr Leu Thr Xaa Ala
305 310 315 320

Ala Met Phe Arg Gly Arg Met Ser Xaa Arg Glu Val Asp Asp Gln Met
325 330 335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro
340 345 350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Xaa Arg Gly Leu Lys
355 360 365

Met Ala Ala Thr Phe Val Gly Asn Xaa Thr Ala Xaa Gln Glu Leu Phe
370 375 380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe
385 390 395 400

Leu His Xaa Tyr Thr Xaa Glu Gly Met Asp Glu Met Glu Phe Thr Glu
405 410 415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln
420 425 430

Glu Ala Xaa Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu
435 440 445

Glu Ala Tyr Pro Glu Glu
450

<210> 5
<211> 1428
<212> DNA
<213> Cylicocyclus nassatus

<220>
<221> CDS
<222> (1)..(1362)
<223>



cgt aaa cta gct gtt aac atg gtt cca ttc cct cgt ctt cac ttc ttt	816
Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe	
260 265 270	
atg cct ggc ttt gct ccc ctc tct gct aaa ggc gct cag gct tac cgt	864
Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg	
275 280 285	
gct ctt act gta gcc gag cta act caa cag atg ttc gat gcc aaa aat	912
Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn	
290 295 300	
atg atg gcc gct tgc gac cct cga cat gga cgt tat ctc acc gtc gca	960
Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala	
305 310 315 320	
gcc atg ttc cga gga cga atg agc atg agg gag gta gac gac cag atg	1008
Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met	
325 330 335	
atg tca gtg cag aac aag aac tcc tca tac ttc gta gag tgg att ccg	1056
Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro	
340 345 350	
aac aac gtc aag acc gct gta tgc gac att ccg ccg aga gga ctg aaa	1104
Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys	
355 360 365	
atg gcc gct acc ttc gtt gga aac tca act gcc atc caa gag ctg ttc	1152
Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe	
370 375 380	
aag cgc att tca gaa caa ttc aca gct atg ttc cgc cgc aaa gcg ttc	1200
Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe	
385 390 395 400	
ttg cat tgg tat act ggt gaa ggt atg gac gag atg gag ttc act gaa	1248
Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu	
405 410 415	
gcc gag tcc aac atg aat gat ctc atc tcc gaa tac cag caa tac cag	1296
Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln	
420 425 430	
gaa gct aca gct gac gat atg ggc gat ctc gat gcg gaa ggc gct gaa	1344
Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu	
435 440 445	
gag gct tac cct gaa gaa tagacagcag attgtgttgc gttgttcggt	1392
Glu Ala Tyr Pro Glu Glu	
450	
tctctgtgtc aatgcgaaat acacattgat tgcggt	1428

<210> 6
 <211> 454
 <212> PRT
 <213> Cylicocyclus nassatus
 <400> 6

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly
 1 5 10 15
 Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp
 20 25 30
 Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu
 35 40 45
 Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys
 50 55 60
 Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp
 65 70 75 80
 Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr
 85 90 95
 Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr
 100 105 110
 Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys
 115 120 125
 Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser
 130 135 140
 Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys
 145 150 155 160
 Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Ser Ser Phe Ser Val Val
 165 170 175
 Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr Asn Ala Thr
 180 185 190
 Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile
 195 200 205
 Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr
 210 215 220
 Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser
 225 230 235 240
 Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu
 245 250 255

Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe
 260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg
 275 280 285

Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn
 290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala
 305 310 315 320

Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met
 325 330 335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro
 340 345 350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys
 355 360 365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe
 370 375 380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe
 385 390 395 400

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu
 405 410 415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln
 420 425 430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu
 435 440 445

Glu Ala Tyr Pro Glu Glu
 450

<210> 7
 <211> 1429
 <212> DNA
 <213> Cylicocyclus nassatus

<220>
 <221> CDS
 <222> (1)..(1362)
 <223>

<400> 7

aag Lys 1	ttc Phe	tct Ser	act Thr	gca Ala 5	ata Ile	atg Met	cgt Arg	gag Glu	atc Ile 10	gtg Val	cat His	gta Val	caa Gln	gct Ala 15	gga Gly	48
cag Gln	tgt Cys	gga Gly	aac Asn 20	caa Gln	att Ile	ggt Gly	tcc Ser	aag Lys 25	ttt Phe	tgg Trp	gaa Glu	gtg Val	atc Ile 30	tct Ser	gac Asp	96
gag Glu	cac His	ggc Gly 35	att Ile	aag Lys	ccc Pro	gat Asp	ggc Gly 40	aca Thr	tac Tyr	cac His	gga Gly 45	gaa Glu	tct Ser	gac Asp	tta Leu	144
caa Gln 50	tta Leu	gaa Glu	cga Arg	atc Ile	aat Asn	gtg Val 55	tac Tyr	tat Tyr	aat Asn	gaa Glu	gca Ala 60	cat His	gga Gly	ggc Gly	aaa Lys	192
tat Tyr 65	gtc Val	ccg Pro	cgt Arg	gca Ala 70	gtt Val	ctt Leu	gtt Val	gat Asp	ctc Leu	gag Glu 75	ccc Pro	gga Gly	act Thr	atg Met	gat Asp 80	240
tcg Ser	gtc Val	cgt Arg	tcc Ser	ggg Gly 85	cca Pro	tac Tyr	ggg Gly	caa Gln	ttg Leu 90	ttc Phe	cgc Arg	cct Pro	gat Asp	aac Asn 95	tac Tyr	288
gtg Val	ttt Phe	gga Gly	cag Gln 100	tct Ser	ggc Gly	gca Ala	gga Gly	aat Asn 105	aac Asn	tgg Trp	gca Ala	aaa Lys	ggg Gly 110	cac His	tac Tyr	336
act Thr	gaa Glu	ggc Gly 115	gct Ala	gaa Glu	ctt Leu	gtc Val	gac Asp 120	aat Asn	gta Val	cta Leu	gat Asp	gta Val 125	gtg Val	cga Arg	aaa Lys	384
gaa Glu 130	gct Ala	gaa Glu	gga Gly	tgt Cys	gac Asp	tgt Cys 135	ctg Leu	cag Gln	ggc Gly	ttc Phe	cag Gln 140	cta Leu	act Thr	cac His	tca Ser	432
ctt Leu 145	gga Gly	gga Gly	ggg Gly	acc Thr	gga Gly 150	tcg Ser	agt Ser	atg Met	ggc Gly	act Thr 155	ctc Leu	ctc Leu	atc Ile	ttc Phe	aaa Lys 160	480
att Ile	cgg Arg	gag Glu	gag Glu	tat Tyr 165	cct Pro	gat Asp	aga Arg	atc Ile	ata Ile 170	tcc Ser	tcg Ser	ttc Phe	ttc Phe	gtt Val 175	gtt Val	528
ccc Pro	tca Ser	cca Pro	aag Lys 180	gtc Val	tcc Ser	gac Asp	acc Thr	gtt Val 185	gtg Val	gag Glu	ccg Pro	tac Tyr	aat Asn 190	gct Ala	acc Thr	576
cta Leu	tcc Ser	gtt Val 195	cat His	cag Gln	ttg Leu	gtt Val	gaa Glu 200	aat Asn	aca Thr	gac Asp	gag Glu	act Thr 205	ttc Phe	tgt Cys	att Ile	624
gac Asp	aat Asn 210	gaa Glu	gct Ala	ctt Leu	tat Tyr	gat Asp 215	att Ile	tgc Cys	ttc Phe	cgc Arg	act Thr 220	ttg Leu	aaa Lys	ctc Leu	acg Thr	672
aac Asn 225	cca Pro	act Thr	tat Tyr	gga Gly	gat Asp 230	ctg Leu	aat Asn	cat His	ctt Leu	gtg Val 235	tct Ser	gta Val	aca Thr	atg Met	tct Ser 240	720
ggg Gly	gtc Val	act Thr	aca Thr	tgt Cys 245	ctt Leu	cgc Arg	ttc Phe	cct Pro	ggc Gly 250	caa Gln	ttg Leu	agt Ser	gcc Ala	gat Asp 255	cta Leu	768

cgt aaa cta gct gtt aac atg gtt cca ttc cct cgt ctt cac ttc ttt	816
Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe	
260 265 270	
atg cct ggc ttt gct ccc ctc tct gct aaa ggc gct cag gct tac cgt	864
Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg	
275 280 285	
gct ctt act gta gcc gag cta act caa cag atg ttc gat gcc aaa aat	912
Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn	
290 295 300	
atg atg gcc gct tgc gac cct cga cat gga cgt tat ctc acc gtc gca	960
Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala	
305 310 315 320	
gcc atg ttc cga gga cga atg agc atg agg gag gta gac gac cag atg	1008
Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met	
325 330 335	
atg tca gtg cag aac aag aac tcc tca tac ttc gta gag tgg att ccg	1056
Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro	
340 345 350	
aac aac gtc aag acc gct gta tgc gac att ccg ccg aga gga ctg aaa	1104
Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys	
355 360 365	
atg gcc gct acc ttc gtt gga aac tca act gcc att caa gag ctg ttc	1152
Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe	
370 375 380	
aag cgc att tca gaa caa ttt aca gct atg ttc cgc cgc aaa gcg ttc	1200
Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe	
385 390 395 400	
ttg cat tgg tat act ggt gaa ggt atg gac gag atg gag ttc act gaa	1248
Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu	
405 410 415	
gcc gag tcc aac atg aat gat ctc atc tcc gaa tac caa caa tac cag	1296
Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln	
420 425 430	
gaa gct acc gct gac gat atg ggc gat ctc gat gcg gaa ggc gct gaa	1344
Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu	
435 440 445	
gag gct tac cct gag gaa tagaacagca gattgtgttg cgttgttcgt	1392
Glu Ala Tyr Pro Glu Glu	
450	
ttctctgtgt caatgcgaaa tacacattga ttgcgtt	1429

<210> 8
 <211> 454
 <212> PRT
 <213> Cylicocyclus nassatus

 <400> 8

Lys Phe Ser Thr Ala Ile Met Arg Glu Ile Val His Val Gln Ala Gly
 1 5 10 15

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp
20 25 30

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu
35 40 45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys
50 55 60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp
65 70 75 80

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr
85 90 95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr
100 105 110

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys
115 120 125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser
130 135 140

Leu Gly Gly Gly Thr Gly Ser Ser Met Gly Thr Leu Leu Ile Phe Lys
145 150 155 160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Ile Ser Ser Phe Phe Val Val
165 170 175

Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu Pro Tyr Asn Ala Thr
180 185 190

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile
195 200 205

Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr
210 215 220

Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser
225 230 235 240

Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Ser Ala Asp Leu
245 250 255

Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe
260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg
 275 280 285

Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn
 290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala
 305 310 315 320

Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met
 325 330 335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro
 340 345 350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys
 355 360 365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe
 370 375 380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe
 385 390 395 400

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu
 405 410 415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln
 420 425 430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu
 435 440 445

Glu Ala Tyr Pro Glu Glu
 450

<210> 9
 <211> 1428
 <212> DNA
 <213> Cylicocyclus nassatus

<220>
 <221> CDS
 <222> (1)..(1362)
 <223>

<400> 9

aag Lys 1	ttc Phe	tct Ser	act Thr	gca Ala 5	ata Ile	atg Met	cgt Arg	gag Glu	atc Ile 10	gtg Val	cat His	gta Val	caa Gln 15	gct Ala 15	gga Gly	48
cag Gln	tgt Cys	gga Gly	aac Asn 20	caa Gln	att Ile	ggt Gly	tcc Ser	aag Lys 25	ttc Phe	tgg Trp	gaa Glu	gtg Val	atc Ile 30	tct Ser	gac Asp	96
gag Glu	cac His	ggc Gly 35	att Ile	aag Lys	ccc Pro	gac Asp	ggc Gly 40	aca Thr	tac Tyr	cat His	gga Gly	gaa Glu 45	tct Ser	gat Asp	cta Leu	144
caa Gln 50	tta Leu	gaa Glu	cga Arg	atc Ile	aat Asn 55	gtg Val 55	tac Tyr	tat Tyr	aat Asn	gaa Glu	gca Ala 60	cat His	gga Gly	ggc Gly	aag Lys	192
tat Tyr 65	gtc Val	ccg Pro	cgt Arg	gca Ala 70	gtt Val 70	ctt Leu	gtt Val	gat Asp	ctc Leu	gag Glu 75	ccc Pro	gga Gly	act Thr	atg Met	gat Asp 80	240
tca Ser	gtc Val	cgt Arg	tct Ser	ggg Gly 85	cca Pro	tac Tyr	ggg Gly	caa Gln	ttg Leu 90	ttc Phe	cgc Arg	cct Pro	gat Asp	aac Asn 95	tac Tyr	288
gtg Val	ttt Phe	gga Gly	cag Gln 100	tct Ser	ggc Gly	gca Ala	gga Gly	aat Asn 105	aac Asn	tgg Trp	gca Ala	aaa Lys	ggt Gly 110	cac His	tac Tyr	336
act Thr	gaa Glu	ggc Gly 115	gct Ala	gaa Glu	ctt Leu	gtc Val	gac Asp 120	aat Asn	gta Val	cta Leu	gat Asp	gta Val 125	gtg Val	cga Arg	aaa Lys	384
gaa Glu 130	gct Ala	gaa Glu	gga Gly	tgt Cys	gac Asp	tgt Cys 135	ctg Leu	cag Gln	ggc Gly	ttc Phe	cag Gln 140	cta Leu	act Thr	cac His	tca Ser	432
ctt Leu 145	gga Gly	gga Gly	ggt Gly	acc Thr	gga Gly 150	tcg Ser	ggt Gly	atg Met	ggc Gly	aca Thr 155	ctc Leu	ctc Leu	atc Ile	tcc Ser	aaa Lys 160	480
att Ile	cgg Arg	gag Glu	gag Glu	tat Tyr 165	cct Pro	gat Asp	aga Arg	atc Ile	atg Met 170	tcc Ser	tcg Ser	ttc Phe	tcc Ser	gtt Val 175	gtt Val	528
ccc Pro	tca Ser	cca Pro	aag Lys 180	gtc Val	ttc Phe	gat Asp	act Thr	gtt Val 185	gtg Val	gag Glu	ccg Pro	tac Tyr	aat Asn 190	gct Ala	acc Thr	576
cta Leu	tcc Ser	gtt Val 195	cat His	cag Gln	ttg Leu	gtt Val	gaa Glu 200	aat Asn	aca Thr	gac Asp	gag Glu	act Thr 205	ttc Phe	tgt Cys	att Ile	624
gac Asp 210	aat Asn	gaa Glu	gct Ala	ctt Leu	tat Tyr	gat Asp 215	att Ile	tgc Cys	ttc Phe	cgc Arg	acc Thr 220	ttg Leu	aaa Lys	ctc Leu	acg Thr	672
aac Asn 225	cca Pro	act Thr	tat Tyr	gga Gly	gat Asp 230	ctg Leu	aat Asn	cat His	ctt Leu	gtg Val 235	tct Ser	gta Val	aca Thr	atg Met	tct Ser 240	720
ggt Gly	gtc Val	act Thr	aca Thr	tgc Cys 245	ctt Leu	cgc Arg	ttc Phe	cct Pro	ggc Gly 250	caa Gln	ttg Leu	aat Asn	gcc Ala	gat Asp 255	cta Leu	768

Gln Cys Gly Asn Gln Ile Gly Ser Lys Phe Trp Glu Val Ile Ser Asp
20 25 30

Glu His Gly Ile Lys Pro Asp Gly Thr Tyr His Gly Glu Ser Asp Leu
35 40 45

Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu Ala His Gly Gly Lys
50 55 60

Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu Pro Gly Thr Met Asp
65 70 75 80

Ser Val Arg Ser Gly Pro Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr
85 90 95

Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr
100 105 110

Thr Glu Gly Ala Glu Leu Val Asp Asn Val Leu Asp Val Val Arg Lys
115 120 125

Glu Ala Glu Gly Cys Asp Cys Leu Gln Gly Phe Gln Leu Thr His Ser
130 135 140

Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys
145 150 155 160

Ile Arg Glu Glu Tyr Pro Asp Arg Ile Met Ser Ser Phe Ser Val Val
165 170 175

Pro Ser Pro Lys Val Phe Asp Thr Val Val Glu Pro Tyr Asn Ala Thr
180 185 190

Leu Ser Val His Gln Leu Val Glu Asn Thr Asp Glu Thr Phe Cys Ile
195 200 205

Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr
210 215 220

Asn Pro Thr Tyr Gly Asp Leu Asn His Leu Val Ser Val Thr Met Ser
225 230 235 240

Gly Val Thr Thr Cys Leu Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu
245 250 255

Arg Lys Leu Ala Val Asn Met Val Pro Phe Pro Arg Leu His Phe Phe
260 265 270

Met Pro Gly Phe Ala Pro Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg
275 280 285

Ala Leu Thr Val Ala Glu Leu Thr Gln Gln Met Phe Asp Ala Lys Asn
290 295 300

Met Met Ala Ala Cys Asp Pro Arg His Gly Arg Tyr Leu Thr Val Ala
305 310 315 320

Ala Met Phe Arg Gly Arg Met Ser Met Arg Glu Val Asp Asp Gln Met
325 330 335

Met Ser Val Gln Asn Lys Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro
340 345 350

Asn Asn Val Lys Thr Ala Val Cys Asp Ile Pro Pro Arg Gly Leu Lys
355 360 365

Met Ala Ala Thr Phe Val Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe
370 375 380

Lys Arg Ile Ser Glu Gln Phe Thr Ala Met Phe Arg Arg Lys Ala Phe
385 390 395 400

Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu Phe Thr Glu
405 410 415

Ala Glu Ser Asn Met Asn Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln
420 425 430

Glu Ala Thr Ala Asp Asp Met Gly Asp Leu Asp Ala Glu Gly Ala Glu
435 440 445

Glu Ala Tyr Pro Glu Glu
450

<210>	11
<211>	2655
<212>	DNA
<213>	Cylicocyclus nassatus

```
<220>
<221> Intron
<222> (1)..(18)
<223>
```

<220>
<221> Intron

<222> (76)..(358)
<223>

<220>
<221> Intron
<222> (496)..(637)
<223>

<220>
<221> Intron
<222> (865)..(1374)
<223>

<220>
<221> Intron
<222> (1666)..(1723)
<223>

<220>
<221> Intron
<222> (1915)..(1966)
<223>

<220>
<221> Intron
<222> (2064)..(2119)
<223>

<220>
<221> Intron
<222> (2306)..(2354)
<223>

<220>
<221> Intron
<222> (2475)..(2523)
<223>

<220>
<221> Intron
<222> (2592)..(2655)
<223>

<400> 11
aagttctcta ctgcaataat gcgtgagatc gtgcatgtac aagctggaca rtgtggaaac 60
caaattggtt ccaaggtrcg gtagtttyrr twktytrytg atcgtaattc sggmgytytr 120
dagtrryttt ttycgytgyy ratgttgcat yrtgttgcga taaascyraa aawtcawwag 180
rcgaggctgt aaaagsactt ytactttttra atmcrvtgta gcagcatgag tcatcrvcac 240
gtttgcagtg sgtttttttat gcgcwgawcc yctcagaaga tgagaatgvc wtccaytgag 300
cwtagartct grcttttctct cgttawctaa ratcaamtta carcrytyca ttttkcagtt 360
ytgggaagtg atctctgacg agcacggcat taagccygay ggcacatacc ayggagaatc 420
tgatytacaa ttagaacgaa tcaatgtgta ctataatgaa gcacatgggt agtcgtayat 480
ccgcttcggt gtytcccmac gcagrccyct tcagttttta taactgyvcg aatatcgvac 540
gggctctttt gcagcggccw ygattacgca ataccayygc yvcygcagtg gcrvtcgvaa 600

aggaagctac cgctgacgat atgggcgatc tcgatgcgga aggcgctgaa gaggcttacc 2580
 ctgargaata gamcagcaga ytgtgttgcg ttgttcgttt ctctrtgtca atgcgaaata 2640
 cacattgatt gcgtt 2655

<210> 48
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> r is a purine (adenine or guanine); y is a pyrimidine (cytosine, thymine, or uracil)

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> n is adenine, cytosine, guanine, thymine, or uracil

<400> 48
 ggncartgyg gnaaycarat 20

<210> 49
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> r is a purine (adenine or guanine); y is a pyrimidine (cytosine, thymine, or uracil)

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> n is adenine, cytosine, guanine, thymine, or uracil

<400> 49
 gaytgyytnc arggnttyca 20

<210> 50
 <211> 20
 <212> DNA
 <213> Synthetic sequence

<220>
 <221> misc_feature

<222> (1)..(20)
<223> r is a purine (adenine or guanine); y is a pyrimidine (cytosine, thymine, or uracil)

<220>
<221> misc_feature
<222> (1)..(20)
<223> n is adenine, cytosine, guanine, thymine, or uracil

<400> 50
tgraanccyt gnarrcartc